

>gi|15126197|gb|AAE73433.1| Sequence 2 from patent US 6242217
gi|21517369|gb|AAM60707.1| Sequence 83 from patent US 6399761
Length = 411

Score = 783 bits (2023), Expect = 0.0
Identities = 410/411 (99%), Positives = 411/411 (100%)

Query: 1 MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVVLYLII 60

MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVVLYLII

Sbjct: 1 MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVVLYLII 60

Query: 61 GATVFKALEQPHEISQRTTIVIQQKQTFISQHSCVNSTELDELIQQIVAAINAGIIPLGNT 120
GATVFKALEQPHEISQRTTIVIQQKQTFISQHSCVNSTELDELIQQIVAAINAGIIPLGNT

Sbjct: 61 GATVFKALEQPHEISQRTTIVIQQKQTFISQHSCVNSTELDELIQQIVAAINAGIIPLGNT 120

Query: 121 SNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180
SNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ

Sbjct: 121 SNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180

Query: 181 LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIIFKHIEGWSALD 240
LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIIFKHIEGWSALD

Sbjct: 181 LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIIFKHIEGWSALD 240

Query: 241 AIYFVVITLTTIGFGDYVAGGS DIEYLDFYKPVVWF WILVGLAYFAAVLSMIGDWLRVIS 300
AIYFVVITLTTIGFGDYVAGGS DIEYLDFYKPVVWF WILVGLAYFAAVLSMIGDWLRVIS

Sbjct: 241 AIYFVVITLTTIGFGDYVAGGS DIEYLDFYKPVVWF WILVGLAYFAAVLSMIGDWLRVIS 300

Query: 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSIKRKL SAELAGNHQ 360
KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSIKRKL SAELAGNHQ

Sbjct: 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSIKRKL SAELAGNHQ 360

Query: 361 ELTPCRRTLSVNHLTNERDVLPLLKTESIYLNGLTPHCAGEEIAVIENTIK 411
ELTPCRRTLSVNHLT+ERDVLPLLKTESIYLNGLTPHCAGEEIAVIENTIK

Sbjct: 361 ELTPCRRTLSVNHLT SERDVLPLLKTESIYLNGLTPHCAGEEIAVIENTIK 411

>gi|15126199|gb|AAE73435.1| Sequence 6 from patent US 6242217
Length = 411

Score = 764 bits (1974), Expect = 0.0
Identities = 394/411 (95%), Positives = 406/411 (98%)

Query: 1 MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVVLYLII 60

MAAPDLLDPKSAAQNSKPRLSFS+KPTVLASRVESD+ INVMKWKTVSTIFLVVVLYLII

Sbjct: 1 MAAPDLLDPKSAAQNSKPRLSFSKPTVLASRVESDSAINVMKWKTVSTIFLVVVLYLII 60

Query: 61 GATVFKALEQPHEISQRTTIVIQQKQTFISQHSCVNSTELDELIQQIVAAINAGIIPLGNT 120
GA VFKALEQP EISQRTTIVIQQKQTFI+QH+CVNSTELDELIQQIVAAINAGIIPLGNT+

Sbjct: 61 GAAVFKALEQPQEISQRTTIVIQQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120

Query: 121 SNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180

SNQ+SHWDLGSSFFFAGTVITIIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ
 Sbjct: 121 SNQVSHWDLGSSFFFAGTVITIIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180

Query: 181 LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIIFKHIEGWSALD 240
 LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPA+IFKHIEGWSALD
 Sbjct: 181 LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIFKHIEGWSALD 240

Query: 241 AIYFVVITLTTIGFGDYVAGGS DIEYLDFYKPVVWF WILVGLAYFAAVLSMIGDWLRVIS 300
 AIYFVVITLTTIGFGDYVAGGS DIEYLDFYKPVVWF WILVGLAYFAAVLSMIGDWLRVIS
 Sbjct: 241 AIYFVVITLTTIGFGDYVAGGS DIEYLDFYKPVVWF WILVGLAYFAAVLSMIGDWLRVIS 300

Query: 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATS IKRKLSAELAGNHQ 360
 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATS+KRKLSAELAGNHQ
 Sbjct: 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVRKRLSAELAGNHQ 360

Query: 361 ELTPCRRTLSVNHLTNERDVLPPLLKTESIYLNGLTPHCAGEEIAVIENIK 411
 ELTPC RTLSVNHLT+ER+VLPPLLK ESIYLNGLTPHCAGE+IAVIEN+K
 Sbjct: 361 ELTPCMRTLSVNHLTSEREVLPPLLKAESIYLNGLTPHCAGEDIAVIENMK 411

>gi|10042828|emb|CAC07711.1| unnamed protein product [Mus sp.]
 Length = 370

Score = 684 bits (1766), Expect = 0.0
 Identities = 356/368 (96%), Positives = 364/368 (98%)

Query: 1 MAAPDLDPKSAAQNSKPRLSFSTKPTVLASRVESDTTINVMWKTVSTIFLVVVLYLII 60
 MAAPDLDPKSAAQNSKPRLSFS+KPTVLASRVESD+ INVMWKTVSTIFLVVVLYLII
 Sbjct: 1 MAAPDLDPKSAAQNSKPRLSFSSKPTVLASRVESD SAINVMWKTVSTIFLVVVLYLII 60

Query: 61 GATVFKALEQPHEISQRTTIVI QKQTFISQHSCVNSTELDELIQQIVAAINAGIIPLGNT 120
 GA VFKALEQP EISQRTTIVI QKQTFI+QH+CVNSTELDELIQQIVAAINAGIIPLGNT+
 Sbjct: 61 GAAVFKALEQPQEISQRTTIVI QKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120

Query: 121 SNQISHWDLGSSFFFAGTVITIIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180
 SNQ+SHWDLGSSFFFAGTVITIIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ
 Sbjct: 121 SNQVSHWDLGSSFFFAGTVITIIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180

Query: 181 LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIIFKHIEGWSALD 240
 LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPA+IFKHIEGWSALD
 Sbjct: 181 LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIFKHIEGWSALD 240

Query: 241 AIYFVVITLTTIGFGDYVAGGS DIEYLDFYKPVVWF WILVGLAYFAAVLSMIGDWLRVIS 300
 AIYFVVITLTTIGFGDYVAGGS DIEYLDFYKPVVWF WILVGLAYFAAVLSMIGDWLRVIS
 Sbjct: 241 AIYFVVITLTTIGFGDYVAGGS DIEYLDFYKPVVWF WILVGLAYFAAVLSMIGDWLRVIS 300

Query: 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATS IKRKLSAELAGNHQ 360
 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATS+KRKLSAELAGNHQ
 Sbjct: 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVRKRLSAELAGNHQ 360

Query: 361 ELTPCRRT 368

ELTPC RT

Sbjct: 361 ELTPCMRT 368

>gi|17917944|gb|AAE85378.1| Sequence 8 from patent US 6309855
Length = 370Score = 681 bits (1758), Expect = 0.0
Identities = 355/368 (96%), Positives = 363/368 (98%)Query: 1 MAAPDLDLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMWKTVSTIFLVVVLYLII 60
MAAPDLDLDPKSAQNSKPRLSFS+KPTVLASRVESD+ INVMWKTVSTIFLVVVLYLII

Sbjct: 1 MAAPDLDLDPKSAQNSKPRLSFSSKPTVLASRVESDSAINVMWKTVSTIFLVVVLYLII 60

Query: 61 GATVFKALEQPHEISQRTTIVIQQKQTFISQHSCVNSTELDELIQQIVAAINAGIIPLGNT 120
GA VFKALEQP EISQRTTIVIQQKQTFI+QH+CVNSTELDELIQQIVAAINAGIIPLGN+

Sbjct: 61 GAAVFKALEQPQEISQRTTIVIQQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120

Query: 121 SNQISHWDLGSSFFFAGTVITIIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180
SNQ+SHWDLGSSFFFAGTVITIIGFGNISPRTEGGKIFCIIYALLGIPL GFLLAGVGDQ

Sbjct: 121 SNQVSHWDLGSSFFFAGTVITIIGFGNISPRTEGGKIFCIIYALLGIPLLEGFLLAGVGDQ 180

Query: 181 LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIFKHIEGWSALD 240
LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPA+IFKHIEGWSALD

Sbjct: 181 LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIFKHIEGWSALD 240

Query: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS 300
AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS

Sbjct: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS 300

Query: 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSIKRKLSAELAGNHQ 360
KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATS+KRKLSAELAGNHQ

Sbjct: 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHQ 360

Query: 361 ELTPCRRT 368

ELTPC RT

Sbjct: 361 ELTPCMRT 368

INSTANT

SEQ ID NO:4

gi|15126199|gb|AAE73435.1| Sequence 6 from patent US 6242217
 Length = 411

Score = 784 bits (2025), Expect = 0.0
 Identities = 410/411 (99%), Positives = 410/411 (99%)

Query: 1 MAAPDLLDPKSAQNSKPRLSFSSKPTVLASRVESDSAINVMWKTVSTIFLVVVLYI 60
 MAAPDLLDPKSAQNSKPRLSFSSKPTVLASRVESDSAINVMWKTVSTIFLVVVLYI

Sbjct: 1 MAAPDLLDPKSAQNSKPRLSFSSKPTVLASRVESDSAINVMWKTVSTIFLVVVLYI 60

Query: 61 GAAVFKALEQPQEISQRTTIVIQQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120
 GAAVFKALEQPQEISQRTTIVIQQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS

Sbjct: 61 GAAVFKALEQPQEISQRTTIVIQQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120

Query: 121 SNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180
 SNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ

Sbjct: 121 SNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180

Query: 181 LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIFKHIEGWSALD 240
 LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIFKHIEGWSALD

Sbjct: 181 LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIFKHIEGWSALD 240

Query: 241 AIYFVVITLTTIGFGDYVAGGS DIEYLDFYKPVVWF WILVGLAYFAAVLSMIGDWLRVIS 300
 AIYFVVITLTTIGFGDYVAGGS DIEYLDFYKPVVWF WILVGLAYFAAVLSMIGDWLRVIS

Sbjct: 241 AIYFVVITLTTIGFGDYVAGGS DIEYLDFYKPVVWF WILVGLAYFAAVLSMIGDWLRVIS 300

Query: 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHQ 360
 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHQ

Sbjct: 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHQ 360

Query: 361 ELTPCRRTLSVNHLT SEREVLPLLKAESIYLNGLTPHCAGEDIAVIENMK 411
 ELTPC RTLSVNHLT SEREVLPLLKAESIYLNGLTPHCAGEDIAVIENMK

Sbjct: 361 ELTPCMRTLSVNHLT SEREVLPLLKAESIYLNGLTPHCAGEDIAVIENMK 411

>gi|15126197|gb|AAE73433.1| Sequence 2 from patent US 6242217

gi|21517369|gb|AAM60707.1| Sequence 83 from patent US 6399761

Length = 411

Score = 768 bits (1984), Expect = 0.0
 Identities = 396/411 (96%), Positives = 407/411 (99%)

Query: 1 MAAPDLLDPKSAQNSKPRLSFSSKPTVLASRVESDSAINVMWKTVSTIFLVVVLYI 60
 MAAPDLLDPKSAQNSKPRLSFS+KPTVLASRVESD+ INVVMWKTVSTIFLVVVLYI

Sbjct: 1 MAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVVMWKTVSTIFLVVVLYI 60

Query: 61 GAAVFKALEQPQEISQRTTIVIQQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120
 GA VFKALEQP EISQRTTIVIQQTFI+QH+CVNSTELDELIQQIVAAINAGIIPLGNS+

Sbjct: 61 GATVFKALEQPHEISQRTTIVIQQTFISQHSCVNSTELDELIQQIVAAINAGIIPLGNT 120

Query: 121 SNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180

SNQ+SHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ
Sbjct: 121 SNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180

Query: 181 LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIFKHIEGWSALD 240
LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPA+IFKHIEGWSALD
Sbjct: 181 LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIIFKHIEGWSALD 240

Query: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS 300
AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS
Sbjct: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS 300

Query: 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVRKLSAELAGNHQ 360
KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATS+KRKLSAELAGNHQ
Sbjct: 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSIKRKLSAELAGNHQ 360

Query: 361 ELTPCRRTLSVNHLTSERVLPPPLLKAESIYLNGLTPHCAGEDIAVIENMK 411
ELTPCRRTLSVNHLTSER+VLPPPLL ESIYLNGLTPHCAGE+IAVIEN+K
Sbjct: 361 ELTPCRRTLSVNHLTSERDVLPPLLKTESIYLNGLTPHCAGEEIAVIENIK 411

>gi|10042828|emb|CAC07711.1| unnamed protein product [Mus sp.]
Length = 370

Score = 696 bits (1797), Expect = 0.0
Identities = 367/368 (99%), Positives = 367/368 (99%)

Query: 1 MAAPDLDLDPKSAQNSKPRLSFSSKPTVLASRVESDSAINVMWKTVSTIFLVVVLYLI 60
MAAPDLDLDPKSAQNSKPRLSFSSKPTVLASRVESDSAINVMWKTVSTIFLVVVLYLI
Sbjct: 1 MAAPDLDLDPKSAQNSKPRLSFSSKPTVLASRVESDSAINVMWKTVSTIFLVVVLYLI 60

Query: 61 GAAVFKALEQPQEISQRTTIVIQQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPGNS 120
GAAVFKALEQPQEISQRTTIVIQQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPGNS
Sbjct: 61 GAAVFKALEQPQEISQRTTIVIQQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPGNS 120

Query: 121 SNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180
SNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ
Sbjct: 121 SNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180

Query: 181 LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIFKHIEGWSALD 240
LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIFKHIEGWSALD
Sbjct: 181 LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIFKHIEGWSALD 240

Query: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS 300
AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS
Sbjct: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS 300

Query: 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVRKLSAELAGNHQ 360
KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVRKLSAELAGNHQ
Sbjct: 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVRKLSAELAGNHQ 360

Query: 361 ELTPCRRT 368

ELTPC RT

Sbjct: 361 ELTPCMRT 368

>gi|17917944|gb|AAE85378.1| Sequence 8 from patent US 6309855
Length = 370

Score = 693 bits (1789), Expect = 0.0

Identities = 366/368 (99%), Positives = 366/368 (99%)

Query: 1 MAAPDLDLDPKSAQNSKPRLSFSSKPTVLASRVESDSAINVMWKTVSTIFLVVVLYLII 60
MAAPDLDLDPKSAQNSKPRLSFSSKPTVLASRVESDSAINVMWKTVSTIFLVVVLYLII

Sbjct: 1 MAAPDLDLDPKSAQNSKPRLSFSSKPTVLASRVESDSAINVMWKTVSTIFLVVVLYLII 60

Query: 61 GAAVFKALEQPQEISQRTTIVIQQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120
GAAVFKALEQPQEISQRTTIVIQQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS

Sbjct: 61 GAAVFKALEQPQEISQRTTIVIQQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120

Query: 121 SNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180
SNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPL FGFLAGVGDQ

Sbjct: 121 SNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180

Query: 181 LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIFKHIEGWSALD 240
LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIFKHIEGWSALD

Sbjct: 181 LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIFKHIEGWSALD 240

Query: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS 300
AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS

Sbjct: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS 300

Query: 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHQ 360
KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHQ

Sbjct: 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHQ 360

Query: 361 ELTPCRRT 368

ELTPC RT

Sbjct: 361 ELTPCMRT 368

DIFFERENT FROM SEQ ID NO:4 at residue 366:

L5 ANSWER 2 OF 3 DGENE COPYRIGHT 2003 THOMSON DERWENT on STN
ACCESSION NUMBER: AAY28497 Protein DGENE
TITLE: New two pore potassium channel used for, e.g.
treatment of cancer, pulmonary, cardiovascular and inflammatory
diseases
INVENTOR: Chapman C G; Meadows H J
PATENT ASSIGNEE: (SMIK) SMITHKLINE BEECHAM PLC.
PATENT INFO: WO 9937762 A1 19990729 44p
APPLICATION INFO: WO 1998-EP7805 19981202
PRIORITY INFO: GB 1998-22135 19981009
EP 1998-300570 19980127
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 1999-469126 [39]
CROSS REFERENCES: N-PSDB: AAZ00040
DESCRIPTION: Mouse h-TREK1 polypeptide.
AN AAY28497 Protein DGENE
AA 37 A; 14 R; 14 N; 14 D; 0 B; 5 C; 14 Q; 23 E; 0 Z; 28 G; 7 H;
42 I;
39 L; 23 K; 5 M; 25 F; 14 P; 29 S; 27 T; 8 W; 9 Y; 34 V; 0
Others
SQL 411
SEQ
1 maapd1ldpk saaqnskpr1 sfsskptv1a srvesdsain vmkwktvsti
51 flvvvlylii gaavfkaleq pqeisqr1ti viqkqtfiaq hacvnsteld
===== =====
101 eliqqivaai nagiiplgns snqvshwd1g ssffffagtvi ttigfgnisp
151 rteggkifci iyallgiplf gfl1lagvgdq lgtifgkgia kvedtfikwn
201 vsqtkiriis tiifilfgcv lfvalpavif khiegwsald aiyfvvitlt
251 tigfgdyvag gsdieyldfy kpvvwf1wilv glayfaavls migdwlrv1s
301 kktkeevgef rahaaewtan vtaefketrr rlsveiydkf qratsvkrkl
351 saelagnhnq eltpcmrt1s vnhltser1v lpp11kaesi yl1ng1tphca
401 gediavienm k
HITS AT: 65-76

1 maapd1ldpk saaqnskpr1 sfsskptv1a srvesdsain vmkwktvsti
51 flvvvlylii gaavfkaleq pqeisqr1ti viqkqtfiaq hacvnsteld
101 eliqqivaai nagiiplgns snqvshwd1g ssffffagtvi ttigfgnisp
151 rteggkifci iyallgiplf gfl1lagvgdq lgtifgkgia kvedtfikwn
201 vsqtkiriis tiifilfgcv lfvalpavif khiegwsald aiyfvvitlt
251 tigfgdyvag gsdieyldfy kpvvwf1wilv glayfaavls migdwlrv1s
301 kktkeevgef rahaaewtan vtaefketrr rlsveiydkf qratsvkrkl
351 saelagnhnq eltpcmrt1s vnhltser1v lpp11kaesi yl1ng1tphca
401 gediavienm k

L11 ANSWER 23 OF 33 PCTFULL COPYRIGHT 2003 Univentio on STN
ACCESSION NUMBER: 2001046258 PCTFULL ED 20020827
TITLE (ENGLISH): TRANSPORTERS AND ION CHANNELS
TITLE (FRENCH): TRANSPORTEURS ET CANAUX IONIQUES
INVENTOR(S): BAUGHN, Mariah, R.;
BURFORD, Neil;
AU-YOUNG, Janice;
LU, Dyung, Aina, M.;
YANG, Junming;
REDDY, Roopa;
LAL, Preeti;
HILLMAN, Jennifer, L.;
AZIMZAI, Yalda;
YUE, Henry;
NGUYEN, Dannie, B.;
YAO, Monique, G.;
GANDHI, Ameena, R.;
TANG, Y., Tom;
KHAN, Farrah, A.
PATENT ASSIGNEE(S): INCYTE GENOMICS, INC.;
BAUGHN, Mariah, R.;
BURFORD, Neil;
AU-YOUNG, Janice;
LU, Dyung, Aina, M.;
YANG, Junming;
REDDY, Roopa;
LAL, Preeti;
HILLMAN, Jennifer, L.;
AZIMZAI, Yalda;
YUE, Henry;
NGUYEN, Dannie, B.;
YAO, Monique, G.;
GANDHI, Ameena, R.;
TANG, Y., Tom;
KHAN, Farrah, A.
DOCUMENT TYPE: Patent
PATENT INFORMATION:
NUMBER KIND DATE

WO 2001046258 A2 20010628
DESIGNATED STATES
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU
CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN
IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK
MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM
TR TT TZ UA UG US UZ VN YU ZA ZW GH GM KE LS MW MZ SD
SL SZ TZ UG ZW AM AZ BY KG KZ MD RU TJ TM AT BE CH CY
DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR BF BJ CF
CG CI CM GA GN GW ML MR NE SN TD TG
APPLICATION INFO.: WO 2000-US35095 A 20001222
PRIORITY INFO.: US 1999-60/172,000 19991223
US 2000-60/176,083 20000114
US 2000-60/177,332 20000121
US 2000-60/178,572 20000128
US 2000-60/179,758 20000202
US 2000-60/181,625 20000210

L6 ANSWER 4 OF 4 MEDLINE on STN DUPLICATE 2
ACCESSION NUMBER: 1999254548 MEDLINE
DOCUMENT NUMBER: 99254548 PubMed ID: 10321245
TITLE: Inhalational anesthetics activate two-pore-domain
background K⁺ channels.
AUTHOR: Patel A J; Honore E; Lesage F; Fink M; Romey G; Lazdunski M
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et
Cellulaire-CNRS-UPR 411, Valbonne, France.
SOURCE: NATURE NEUROSCIENCE, (1999 May) 2 (5) 422-6.
Journal code: 9809671. ISSN: 1097-6256.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199905
ENTRY DATE: Entered STN: 19990607
Last Updated on STN: 19990607
Entered Medline: 19990525
AB Volatile anesthetics produce safe, reversible unconsciousness, amnesia and analgesia via hyperpolarization of mammalian neurons. In molluscan pacemaker neurons, they activate an inhibitory synaptic K⁺ current (IK_A), proposed to be important in general anesthesia. Here we show that TASK and TREK-1, two recently cloned mammalian two-P-domain K⁺ channels similar to IK_A in biophysical properties, are activated by volatile general anesthetics. Chloroform, diethyl ether, halothane and isoflurane activated TREK-1, whereas only halothane and isoflurane activated TASK. Carboxy (C)-terminal regions were critical for anesthetic activation in both channels. Thus both TREK-1 and TASK are possibly important target sites for these agents.

L17 ANSWER 16 OF 84 MEDLINE

ACCESSION NUMBER: 95355355 MEDLINE

DOCUMENT NUMBER: 95355355 PubMed ID: 7629068

TITLE: Amino terminus and the first four membrane-spanning segments of the *Arabidopsis* K⁺ channel KAT1 confer inward-rectification property of plant-animal chimeric channels.

AUTHOR: Cao Y; Crawford N M; Schroeder J I

CORPORATE SOURCE: Department of Biology, University of California at San Diego, La Jolla 92093-0116, USA.

CONTRACT NUMBER: GM40672 (NIGMS)

SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1995 Jul 28)
270 (30) 17697-701.

JOURNAL code: HIV; 2985121R. ISSN: 0021-9258.

PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199509

ENTRY DATE: Entered STN: 19950921

Last Updated on STN: 19990129

Entered Medline: 19950905

AB The *Arabidopsis* hyperpolarization-activated (inward-rectifying) K⁺ channel KAT1 is structurally more similar to animal depolarization-activated (outward-rectifying) K⁺ channels than to animal hyperpolarization-activated K⁺ channels. To gain insight into the structural basis for the opposite voltage dependences of plant inward-rectifying and animal outward-rectifying K⁺ channels, we constructed recombinant chimeric channels between the hyperpolarization-activated K⁺ channel KAT1 and a *Xenopus* depolarization-activated K⁺ channel. We report here that two of the chimeric constructs, which contain the first third of the KAT1 sequence, including the first four membrane-spanning segments

(S1-S4)

and the linker sequence between the fourth and fifth membrane-spanning segments, express functional channels that retain activation by hyperpolarization, but not depolarization. These two chimeric channels are no longer selective for K⁺. The chimeras are selective for cations over anions and are permeable to Ca²⁺. Therefore, unlike animal hyperpolarization-activated K⁺ channels, in which the carboxyl terminus is important for inward rectification induced by Mg²⁺ and polyamine block, the plant KAT1 channel has its major determinants for inward rectification in the amino-terminal region, which ends at the end of the S4-S5 linker.

WEST

End of Result Set

 Generate Collection

11/15/96

L1: Entry 2 of 2

File: USPT

Jan 11, 2000

US-PAT-NO: 6013470

DOCUMENT-IDENTIFIER: US 6013470 A

TITLE: Family of mammalian potassium channels, their cloning and their use especially for the screening of drugs

DATE-ISSUED: January 11, 2000

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Lesage; Florian	Nice			FR
Guillemare; Eric	Nice			FR
Fink; Michel	Cannes La Bocca			FR
Duprat; Fabrice	Valluris			FR
Lazdunski; Michel	Nice			FR
Romey; Georges	Nice			FR
Barhanin; Jacques	Nice			FR

US-CL-CURRENT: 435/69.1; 435/320.1, 435/325, 536/23.1

CLAIMS:

We claim:

1. An isolated and purified nucleic acid molecule encoding a mammalian protein which comprises 2 P domains and 4 transmembrane segments, and is competent to transport potassium across a membrane.
2. An isolated and purified nucleic acid molecule encoding a human protein which comprises 2 P domains and 4 transmembrane segments, and is competent to transport potassium across a membrane.
3. The nucleic acid molecule of claim 2 encoding a human protein which exhibits weak inward rectification.
4. The nucleic acid molecule of claim 3 which is expressed in brain and heart tissue and in addition, in at least one of the following tissues: placenta, liver, skeletal, muscle, kidney and pancreas.
5. The human nucleic acid sequence of claim 2 which comprises the sequence represented by SEQ ID No. 1. *Encodes SEQ ID NO: 5*
6. A self replication vector comprising the nucleic acid molecule of claim 2.
7. A cell transformed with the self replicating vector of claim 6, which cell expresses a human protein which comprises 2 P domains and 4 transmembrane segments, and is competent to transport potassium across a membrane.
8. A micro-injected cell comprising the RNA transcript synthesized from the nucleic acid molecule of claim 2, which cell expresses a human protein which

comprises 2 P domains and 4 transmembrane segments, and is competent to transport potassium across a membrane.

9. The transformed cell of claim 7, which cell is selected from the group consisting of prokaryotes and eukaryotes.

10. The transformed cell of claim 9 which is a bacterium.

11. The transformed cell of claim 10 which is a yeast, insect, plant or mammalian cell.

12. A method for the production of a human protein competent to transport potassium across a membrane which comprises 2 P domains and 4 transmembrane segments, comprising transferring the vector of claim 6 into a cellular host, culturing the cellular host under conditions allowing the production of said potassium channel, and purifying the human potassium channel.

13. The method of claim 12 wherein the cellular host is selected from the group consisting of prokaryotes and eukaryotes.

14. A pharmaceutical composition for the compensation of a deficiency in potassium channels at the level of one or more tissues, which comprises an isolated and purified nucleic acid molecule encoding a human protein comprising 2 P domains and 4 transmembrane segments which protein is competent to transport potassium across a membrane.

15. A pharmaceutical composition which comprises human cells transformed with the nucleic acid molecule of claim 2.

WEST

End of Result Set

L4: Entry 1 of 1

File: USPT

Jan 11, 2000

DOCUMENT-IDENTIFIER: US 6013470 A

TITLE: Family of mammalian potassium channels, their cloning and their use especially for the screening of drugs

US Patent No. (1):
6013470

Brief Summary Text (5):

The subunits of the voltage-dependent K^{sup.+} channels activated by depolarization (K_V families) and the calcium-dependent K^{sup.+} channels exhibit six hydrophobic transmembranal domains, one of which (S4) contains repeated positive charges which confer on these channels their sensitivity to voltage and, consequently, in their functional outward rectification (Logothetis, D. E. et al., 1992, *Neuron*, 8, 531-540; Bezanilla, F. and Stefani, E., 1994, *Annu. Rev. Biophys. Biomol. Struct.*, 23, 819-846).